

## SEQUENCE LISTING

<110> Kindsvo gel, Wayne R.  
Topouzis, Stavros

## <120> SOLUBLE ZCYTOR11 CYTOKINE RECEPTORS

<130> 00-56

<150> US 60/223,827

<151> 2000-08-08

<150> US 60/250,876

<151> 2000-12-01

<160> 35

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2831

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (34)...(1755)

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Met Arg Thr Leu Leu Thr Ile  
1 5

54

ttg act gtg gga tcc ctg gct gct cac gcc cct gag gac ccc tcg gat  
Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp  
10 15 20

102

ctg ctc cag cac gtg aaa ttc cag tcc agc aac ttt gaa aac atc ctg  
 Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu  
 25                   30                   35

150

acg tgg gac agc ggg cca gag ggc acc cca gac acg gtc tac agc atc

Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile				
40	45	50	55	
gag tat aag acg tac gga gag agg gac tgg gtg gca aag aag ggc tgt				246
Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys				
60	65	70		
cag cgg atc acc cgg aag tcc tgc aac ctg acg gtg gag acg ggc aac				294
Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn				
75	80	85		
ctc acg gag ctc tac tat gcc agg gtc acc gct gtc agt gcg gga ggc				342
Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly				
90	95	100		
cg <sup>g</sup> tca gcc acc aag atg act gac agg ttc agc tct ctg cag cac act				390
Arg Ser Ala Thr Lys Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr				
105	110	115		
acc ctc aag cca cct gat gtg acc tgt atc tcc aaa gtg aga tcg att				438
Thr Leu Lys Pro Pro Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile				
120	125	130	135	
cag atg att gtt cat cct acc ccc acg cca atc cgt gca ggc gat ggc				486
Gln Met Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly				
140	145	150		
cac cgg cta acc ctg gaa gac atc ttc cat gac ctg ttc tac cac tta				534
His Arg Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu				
155	160	165		
gag ctc cag gtc aac cgc acc tac caa atg cac ctt gga ggg aag cag				582
Glu Leu Gln Val Asn Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln				
170	175	180		
aga gaa tat gag ttc ttc ggc ctg acc cct gac aca gag ttc ctt ggc				630
Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly				
185	190	195		
acc atc atg att tgc gtt ccc acc tgg gcc aag gag agt gcc ccc tac				678
Thr Ile Met Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr				
200	205	210	215	

atg tgc cga gtg aag aca ctg cca gac cg	acc tac tcc ttc	726	
Met Cys Arg Val Lys Thr Leu Pro Asp Arg	Thr Trp Thr Tyr Ser Phe		
220	225	230	
tcc gga gcc ttc ctg ttc tcc atg ggc ttc	ctc gtc gca gta ctc tgc	774	
Ser Gly Ala Phe Leu Phe Ser Met Gly Phe	Leu Val Ala Val Leu Cys		
235	240	245	
tac ctg agc tac aga tat gtc acc aag ccg	cct gca cct ccc aac tcc	822	
Tyr Leu Ser Tyr Arg Tyr Val Thr Lys Pro	Pro Ala Pro Pro Asn Ser		
250	255	260	
ctg aac gtc cag cga gtc ctg act ttc cag	ccg ctg cgc ttc atc cag	870	
Leu Asn Val Gln Arg Val Leu Thr Phe Gln	Pro Leu Arg Phe Ile Gln		
265	270	275	
gag cac gtc ctg atc cct gtc ttt gac ctc	agg ccc agc agt ctg	918	
Glu His Val Leu Ile Pro Val Phe Asp Leu	Ser Gly Pro Ser Ser Leu		
280	285	290	295
gcc cag cct gtc cag tac tcc cag atc agg	gtg tct gga ccc agg gag	966	
Ala Gln Pro Val Gln Tyr Ser Gln Ile Arg	Val Ser Gly Pro Arg Glu		
300	305	310	
ccc gca gga gct cca cag ccg cat agc ctg	tcc gag atc acc tac tta	1014	
Pro Ala Gly Ala Pro Gln Arg His Ser Leu	Ser Glu Ile Thr Tyr Leu		
315	320	325	
ggg cag cca gac atc tcc atc ctc cag	ccc tcc aac gtg cca cct ccc	1062	
Gly Gln Pro Asp Ile Ser Ile Leu Gln Pro	Ser Asn Val Pro Pro Pro		
330	335	340	
cag atc ctc tcc cca ctg tcc tat gcc	cca aac gct gcc cct gag gtc	1110	
Gln Ile Leu Ser Pro Leu Ser Tyr Ala Pro	Asn Ala Ala Pro Glu Val		
345	350	355	
ggg ccc cca tcc tat gca cct cag gtg	acc ccc gaa gct caa ttc cca	1158	
Gly Pro Pro Ser Tyr Ala Pro Gln Val Thr	Pro Glu Ala Gln Phe Pro		
360	365	370	375
ttc tac gcc cca cag gcc atc tct aag gtc	cag cct tcc tat gcc	1206	
Phe Tyr Ala Pro Gln Ala Ile Ser Lys Val	Gln Pro Ser Ser Tyr Ala		
380	385	390	

cct caa gcc act ccg gac agc tgg cct ccc tcc tat ggg gta tgc atg Pro Gln Ala Thr Pro Asp Ser Trp Pro Pro Ser Tyr Gly Val Cys Met	395	400	405	1254
gaa ggt tct ggc aaa gac tcc ccc act ggg aca ctt tct agt cct aaa Glu Gly Ser Gly Lys Asp Ser Pro Thr Gly Thr Leu Ser Ser Pro Lys	410	415	420	1302
cac ctt agg cct aaa ggt cag ctt cag aaa gag cca cca gct gga agc His Leu Arg Pro Lys Gly Gln Leu Gln Lys Glu Pro Pro Ala Gly Ser	425	430	435	1350
tgc atg tta ggt ggc ctt tct ctg cag gag gtg acc tcc ttg gct atg Cys Met Leu Gly Leu Ser Leu Gln Glu Val Thr Ser Leu Ala Met	440	445	450	455
gag gaa tcc caa gaa gca aaa tca ttg cac cag ccc ctg ggg att tgc Glu Glu Ser Gln Glu Ala Lys Ser Leu His Gln Pro Leu Gly Ile Cys	460	465	470	1446
aca gac aga aca tct gac cca aat gtg cta cac agt ggg gag gaa ggg Thr Asp Arg Thr Ser Asp Pro Asn Val Leu His Ser Gly Glu Gly	475	480	485	1494
aca cca cag tac cta aag ggc cag ctc ccc ctc ctc tcc tca gtc cag Thr Pro Gln Tyr Leu Lys Gly Gln Leu Pro Leu Leu Ser Ser Val Gln	490	495	500	1542
atc gag ggc cac ccc atg tcc ctc cct ttg caa cct cct tcc ggt cca Ile Glu Gly His Pro Met Ser Leu Pro Leu Gln Pro Pro Ser Gly Pro	505	510	515	1590
tgt tcc ccc tcg gac caa ggt cca agt ccc tgg ggc ctg ctg gag tcc Cys Ser Pro Ser Asp Gln Gly Pro Ser Pro Trp Gly Leu Leu Glu Ser	520	525	530	535
ctt gtg tgt ccc aag gat gaa gcc aag agc cca gcc cct gag acc tca Leu Val Cys Pro Lys Asp Glu Ala Lys Ser Pro Ala Pro Glu Thr Ser	540	545	550	1686
gac ctg gag cag ccc aca gaa ctg gat tct ctt ttc aga ggc ctg gcc				1734

Asp Leu Glu Gln Pro Thr Glu Leu Asp Ser Leu Phe Arg Gly Leu Ala  
 555 560 565

ctg act gtg cag tgg gag tcc tgaggggaaat gggaaaggct tggtgcttcc 1785  
 Leu Thr Val Gln Trp Glu Ser  
 570

tccctgtccc tacccagtgt cacatccttg gctgtcaatc ccatgcctgc ccatgccaca 1845  
 cactctgcga tctggcctca gacgggtgcc cttgagagaa gcagagggag tggcatgcag 1905  
 gccccctgcc atgggtgcgc tcctcaccgg aacaaagcag catgataagg actgcagcgg 1965  
 gggagctctg gggagcagct tggtagaca agcgcgtgct cgctgagccc tgcaaggcag 2025  
 aaatgacagt gcaaggagga aatgcagggaa aactcccgag gtccagagcc ccaccccta 2085  
 acaccatgga ttcaaagtgc tcagggatt tgccttcct tgcccattc ctggccagtt 2145  
 tcacaatcta gctcgacaga gcatgaggcc cctgcctctt ctgtcattgt tcaaagggtgg 2205  
 gaagagagcc tggaaaagaa ccaggcctgg aaaagaacca gaaggaggct gggcagaacc 2265  
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 tttctgcagg caggagttc agaccctatc ctgagaatgg ggtttaaaag gaaggtgagg 2505  
 gctgtggccc ctggacgggt acaataaacac actgtactga tgtcacaact ttgcaagctc 2565  
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 cttcaaacaa atgaaatcag tgcccaacac ctcgggttcc tcatctgtaa tgtgggatc 2685  
 ataacaccta cctcatggag ttgtggtaa gatgaaatga agtcatgtct taaaagtgtc 2745  
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 aaaaaaaaaa atagcggccg cctcga 2831

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<211> 574  
<212> PRT  
<213> Homo sapien

<400> 2

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Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser  
 20 25 30

Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr  
 35 40 45

Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp  
 50 55 60

Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn  
 65 70 75 80

Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val  
                   85                  90                  95  
 Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg  
                   100              105                  110  
 Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys  
                   115              120                  125  
 Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr  
                   130              135              140  
 Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe  
                   145              150              155                  160  
 His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln  
                   165              170                  175  
 Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr  
                   180              185                  190  
 Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp  
                   195              200                  205  
 Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp  
                   210              215                  220  
 Arg Thr Trp Thr Tyr Ser Phe Ser Gly Ala Phe Leu Phe Ser Met Gly  
                   225              230              235                  240  
 Phe Leu Val Ala Val Leu Cys Tyr Leu Ser Tyr Arg Tyr Val Thr Lys  
                   245              250                  255  
 Pro Pro Ala Pro Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe  
                   260              265                  270  
 Gln Pro Leu Arg Phe Ile Gln Glu His Val Leu Ile Pro Val Phe Asp  
                   275              280                  285  
 Leu Ser Gly Pro Ser Ser Leu Ala Gln Pro Val Gln Tyr Ser Gln Ile  
                   290              295                  300  
 Arg Val Ser Gly Pro Arg Glu Pro Ala Gly Ala Pro Gln Arg His Ser  
                   305              310              315                  320  
 Leu Ser Glu Ile Thr Tyr Leu Gly Gln Pro Asp Ile Ser Ile Leu Gln  
                   325              330                  335  
 Pro Ser Asn Val Pro Pro Pro Gln Ile Leu Ser Pro Leu Ser Tyr Ala  
                   340              345                  350  
 Pro Asn Ala Ala Pro Glu Val Gly Pro Pro Ser Tyr Ala Pro Gln Val  
                   355              360                  365  
 Thr Pro Glu Ala Gln Phe Pro Phe Tyr Ala Pro Gln Ala Ile Ser Lys  
                   370              375                  380  
 Val Gln Pro Ser Ser Tyr Ala Pro Gln Ala Thr Pro Asp Ser Trp Pro  
                   385              390              395                  400  
 Pro Ser Tyr Gly Val Cys Met Glu Gly Ser Gly Lys Asp Ser Pro Thr  
                   405              410                  415

Gly Thr Leu Ser Ser Pro Lys His Leu Arg Pro Lys Gly Gln Leu Gln  
 420 425 430  
 Lys Glu Pro Pro Ala Gly Ser Cys Met Leu Gly Gly Leu Ser Leu Gln  
 435 440 445  
 Glu Val Thr Ser Leu Ala Met Glu Glu Ser Gln Glu Ala Lys Ser Leu  
 450 455 460  
 His Gln Pro Leu Gly Ile Cys Thr Asp Arg Thr Ser Asp Pro Asn Val  
 465 470 475 480  
 Leu His Ser Gly Glu Glu Gly Thr Pro Gln Tyr Leu Lys Gly Gln Leu  
 485 490 495  
 Pro Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Met Ser Leu Pro  
 500 505 510  
 Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln Gly Pro Ser  
 515 520 525  
 Pro Trp Gly Leu Leu Glu Ser Leu Val Cys Pro Lys Asp Glu Ala Lys  
 530 535 540  
 Ser Pro Ala Pro Glu Thr Ser Asp Leu Glu Gln Pro Thr Glu Leu Asp  
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 Ser Leu Phe Arg Gly Leu Ala Leu Thr Val Gln Trp Glu Ser  
 565 570

<210> 3  
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 <212> PRT  
 <213> Homo sapiens

<400> 3  
 Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser Ser  
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 Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp  
 35 40 45  
 Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu  
 50 55 60  
 Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr  
 65 70 75 80  
 Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg Phe  
 85 90 95  
 Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys Ile  
 100 105 110

Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr Pro  
115 120 125  
Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe His  
130 135 140  
Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln Met  
145 150 155 160  
His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro  
165 170 175  
Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp Ala  
180 185 190  
Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp Arg  
195 200 205  
Thr Trp Thr  
210

<210> 4  
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<212> PRT  
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<223> Glu-Glu peptide tag

<400> 4  
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<210> 5  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Flag-tag peptide

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Asp Tyr Lys Asp Asp Asp Asp Lys  
1 5

<210> 6  
<211> 699  
<212> DNA

<213> Homo sapiens

<400> 6

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ggggcaccgt cagtcttcct ctcccccca aaacccaagg acaccctcat gatctcccg	120
accctgagg tcacatgcgt ggtgggtggac gtgagccacg aagaccctga ggtcaagttc	180
aactggtaacg tggacggcgt ggaggtgcat aatgccaaga caaagccgacg ggaggaggcag	240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgaccaggta ctggctgaat	300
ggcaaggagt acaagtcaa ggtctccaac aaagccctcc catcctccat cgagaaaacc	360
atctccaaag ccaaaggggca gccccgagaa ccacaggtgt acaccctgccc cccatcccg	420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc	480
gacatcgccg tggagtgga gagcaatggg cagccggaga acaactacaa gaccacgcct	540
cccgctgg actccgacgg ctcccttcctc ctctacagca agctaccgt ggacaagagc	600
aggtggcagc aggggaacgt ctctcatgc tccgtatgc atgaggctct gcacaaccac	660
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<212> DNA

<213> homo sapiens

<220>

<221> CDS

<222> (21)...(557)

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1 5 10	

ctt atg ggg acc ctg gcc acc agc tgc ctc ctt ctc ttg gcc ctc ttg	101
Leu Met Gly Thr Leu Ala Thr Ser Cys Leu Leu Leu Ala Leu Leu	
15 20 25	

gta cag gga gga gca gct gcg ccc atc agc tcc cac tgc agg ctt gac	149
Val Gln Gly Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp	
30 35 40	

aag tcc aac ttc cag cag ccc tat atc acc aac cgc acc ttc atg ctg	197
Lys Ser Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu	
45 50 55	

gct aag gag gct agc ttg gct gat aac aac aca gac gtt ctc att	245
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Ala Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile			
60	65	70	75
ggg gag aaa ctg ttc cac gga gtc agt atg agt gag cgc tgc tat ctg			293
Gly Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu			
80	85	90	
atg aag cag gtg ctg aac ttc acc ctt gaa gaa gtg ctg ttc cct caa			341
Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln			
95	100	105	
tct gat agg ttc cag cct tat atg cag gag gtg gtg ccc ttc ctg gcc			389
Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala			
110	115	120	
agg ctc agc aac agg cta agc aca tgt cat att gaa ggt gat gac ctg			437
Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu			
125	130	135	
cat atc cag agg aat gtg caa aag ctg aag gac aca gtg aaa aag ctt			485
His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu			
140	145	150	155
gga gag agt gga gag atc aaa gca att gga gaa ctg gat ttg ctg ttt			533
Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe			
160	165	170	
atg tct ctg aga aat gcc tgc att tgaccagagc aaagctgaaa aatgaataac			587
Met Ser Leu Arg Asn Ala Cys Ile			
175			
taacccctt tccctgctag aaataacaat tagatcccc aaagcgattt ttttaacca			647
aaaggaagat gggagccaa actccatcat gatgggtgga ttccaaatga acccctgcgt			707
tagttacaaa ggaaaccaat gccactttt gttataagac cagaaggttag actttctaag			767
catagatatt tattgataac atttcattgt aactgggttt ctatacacag aaaacaattt			827
atttttaaa taattgtctt ttccataaaa aaagattact ttccattcct ttagggaaaa			887
aaacccctaa atagcttcat gttccataa tcagtacttt atattataa atgtatttat			947
tattattata agactgcatt ttatttatat catttatta atatggattt atttataagaa			1007
acatcattcg atattgctac ttgagtgtaa ggctaattt gatattatg acaataatta			1067
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&lt;210&gt; 8

&lt;211&gt; 179

<212> PRT

<213> homo sapiens

<400> 8

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 Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln  
 35 40 45  
 Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser  
 50 55 60  
 Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe  
 65 70 75 80  
 His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu  
 85 90 95  
 Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln  
 100 105 110  
 Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg  
 115 120 125  
 Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn  
 130 135 140  
 Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu  
 145 150 155 160  
 Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn  
 165 170 175  
 Ala Cys Ile

<210> 9

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide prime ZC28590

<400> 9

ttgggtacct ctgcaatggc cgccctgcag aaatct

36

<210> 10

<211> 33

<212> DNA

<213> Artificial Sequence

<220>  
<223> Oligonucleotide prime ZC28580

<400> 10  
ttggatcca atgcaggcat ttctcagaga cat 33

<210> 11  
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<212> DNA  
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<220>  
<223> Oligonucleotide prime ZC14666

<400> 11  
agccaccaag atgactga 18

<210> 12  
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<212> DNA  
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<223> Oligonucleotide prime ZC14742

<400> 12  
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<210> 13  
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<212> PRT  
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<400> 13  
His His His His His His  
1 5

<210> 14  
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<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC29239

<400> 14

gaggccggat ccgggttcggg ttccgggttcg gagcccagat catcagacaa aactcacaca  
tgc

60

63

<210> 15

<211> 65

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC29232

<400> 15

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gggag

60

65

<210> 16

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC39319

<400> 16

atcggaaattc gcagaagcca tggcgtggag ctttggg

37

<210> 17

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC39325

<400> 17

cagtggatcc ggaggggacc gtttcgtc

28

<210> 18  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)...(660)

<400> 18

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1	5			10								15				

gca	ttg	gga	atg	gta	cca	cct	ccc	gaa	aat	gtc	aga	atg	aat	tct	gtt	96
Ala	Leu	Gly	Met	Val	Pro	Pro	Pro	Glu	Asn	Val	Arg	Met	Asn	Ser	Val	
	20			25								30				

aat	ttc	aag	aac	att	cta	cag	tgg	gag	tca	cct	gct	ttt	gcc	aaa	ggg	144
Asn	Phe	Lys	Asn	Ile	Leu	Gln	Trp	Glu	Ser	Pro	Ala	Phe	Ala	Lys	Gly	
	35			40								45				

aac	ctg	act	ttc	aca	gct	cag	tac	cta	agt	tat	agg	ata	ttc	caa	gat	192
Asn	Leu	Thr	Phe	Thr	Ala	Gln	Tyr	Leu	Ser	Tyr	Arg	Ile	Phe	Gln	Asp	
	50		55									60				

aaa	tgc	atg	aat	act	acc	ttg	acg	gaa	tgt	gat	ttc	tca	agt	ctt	tcc	240
Lys	Cys	Met	Asn	Thr	Thr	Leu	Thr	Glu	Cys	Asp	Phe	Ser	Ser	Leu	Ser	
	65		70			75		80								

aag	tat	ggt	gac	cac	acc	ttg	aga	gtc	agg	gct	gaa	ttt	gca	gat	gag	288
Lys	Tyr	Gly	Asp	His	Thr	Leu	Arg	Val	Arg	Ala	Glu	Phe	Ala	Asp	Glu	
	85		90									95				

cat	tca	gac	tgg	gta	aac	atc	acc	ttc	tgt	cct	gtg	gat	gac	acc	att	336
His	Ser	Asp	Trp	Val	Asn	Ile	Thr	Phe	Cys	Pro	Val	Asp	Asp	Thr	Ile	
	100		105									110				

att	gga	ccc	cct	gga	atg	caa	gta	gaa	gta	ctt	gat	gat	tct	tta	cat	384
Ile	Gly	Pro	Pro	Gly	Met	Gln	Val	Glu	Val	Leu	Asp	Asp	Ser	Leu	His	
	115		120									125				

atg cgt ttc tta gcc cct aaa att gag aat gaa tac gaa act tgg act		432	
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Thr Trp Thr			
130	135	140	
atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa		480	
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys			
145	150	155	160
aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag		528	
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu			
165	170	175	
gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga		576	
Val Leu Arg Asn Leu Glu Pro Trp Thr Tyr Cys Val Gln Val Arg			
180	185	190	
ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg agt gag cct gtc		624	
Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val			
195	200	205	
tgt gag caa aca acc cat gac gaa acg gtc ccc tcc		660	
Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser			
210	215	220	
<210> 19			
<211> 220			
<212> PRT			
<213> Homo sapiens			
<400> 19			
Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser			
1	5	10	15
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val			
20	25	30	
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly			
35	40	45	
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp			
50	55	60	
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser			
65	70	75	80
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu			
85	90	95	

His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile  
     100                 105                 110  
 Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His  
     115                 120                 125  
 Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Thr Trp Thr  
     130                 135                 140  
 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys  
     145                 150                 155                 160  
 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu  
     165                 170                 175  
 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg  
     180                 185                 190  
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val  
     195                 200                 205  
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser  
     210                 215                 220

<210> 20

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC38931

<400> 20

acaaagccgc gggaggag

18

<210> 21

<211> 82

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC39042

<400> 21

ctgactcgag tcagtgtatgg ttagtgtatgg ggccacctga tccggAACCA cgccggAACCA  
gtttacccgg agacaggag ag

60

82

<210> 22

<211> 1428

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1428)

<223> CRF2-4 extracellular cytokine binding domain fused  
to IgG1 with a 6-HIS tag

&lt;400&gt; 22

atg	gcg	tgg	agt	ctt	ggg	agc	tgg	ctg	ggt	ggc	tgc	ctg	gtg	tca		48
Met	Ala	Trp	Ser	Leu	Gly	Ser	Trp	Leu	Gly	Gly	Cys	Leu	Leu	Val	Ser	
1				5				10						15		
gca	ttg	gga	atg	gta	cca	cct	ccc	gaa	aat	gtc	aga	atg	aat	tct	gtt	96
Ala	Leu	Gly	Met	Val	Pro	Pro	Pro	Glu	Asn	Val	Arg	Met	Asn	Ser	Val	
				20				25						30		
aat	ttc	aag	aac	att	cta	cag	tgg	gag	tca	cct	gct	ttt	gcc	aaa	ggg	144
Asn	Phe	Lys	Asn	Ile	Leu	Gln	Trp	Glu	Ser	Pro	Ala	Phe	Ala	Lys	Gly	
				35				40						45		
aac	ctg	act	ttc	aca	gct	cag	tac	cta	agt	tat	agg	ata	ttc	caa	gat	192
Asn	Leu	Thr	Phe	Thr	Ala	Gln	Tyr	Leu	Ser	Tyr	Arg	Ile	Phe	Gln	Asp	
				50				55						60		
aaa	tgc	atg	aat	act	acc	ttg	acg	gaa	tgt	gat	ttc	tca	agt	ctt	tcc	240
Lys	Cys	Met	Asn	Thr	Thr	Leu	Thr	Glu	Cys	Asp	Phe	Ser	Ser	Leu	Ser	
				65				70						75		80
aag	tat	ggt	gac	cac	acc	ttg	aga	gtc	agg	gct	gaa	ttt	gca	gat	gag	288
Lys	Tyr	Gly	Asp	His	Thr	Leu	Arg	Val	Arg	Ala	Glu	Phe	Ala	Asp	Glu	
				85				90						95		
cat	tca	gac	tgg	gta	aac	atc	acc	ttc	tgt	cct	gtg	gat	gac	acc	att	336
His	Ser	Asp	Trp	Val	Asn	Ile	Thr	Phe	Cys	Pro	Val	Asp	Asp	Thr	Ile	
				100				105						110		
att	gga	ccc	cct	gga	atg	caa	gta	gaa	gta	ctt	gat	gat	tct	tta	cat	384
Ile	Gly	Pro	Pro	Gly	Met	Gln	Val	Glu	Val	Leu	Asp	Asp	Ser	Leu	His	
				115				120						125		

atg cgt ttc tta gcc cct aaa att gag aat gaa tac gaa act tgg act Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr 130 135 140	432
atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys 145 150 155 160	480
aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu 165 170 175	528
gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga Val Leu Arg Asn Leu Glu Pro Trp Thr Tyr Cys Val Gln Val Arg 180 185 190	576
ggg ttt ctt cct gat cg <sup>g</sup> aac aaa gct ggg gaa tgg agt gag cct gtc Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val 195 200 205	624
tgt gag caa aca acc cat gac gaa acg gtc ccc tcc gga tcc ggt tcg Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Gly Ser Gly Ser 210 215 220	672
gg <sup>t</sup> tcg ggt tcg gag ccc aga tca tca gac aaa act cac aca tgc cca Gly Ser Gly Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys Pro 225 230 235 240	720
ccg tgc cca gca cct gaa gcc gag ggg gca ccg tca gtc ttc ctc ttc Pro Cys Pro Ala Pro Glu Ala Gly Ala Pro Ser Val Phe Leu Phe 245 250 255	768
ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val 260 265 270	816
aca tgc gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe 275 280 285	864
aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro 290 295 300	912

cg <sup>g</sup> gag gag cag tac aac agc acg tac cgt gt <sup>g</sup> gtc agc gtc ctc acc Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr	305	310	315	320	960
gt <sup>c</sup> ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val	325	330	335		1008
tcc aac aaa gcc ctc cca tcc tcc atc gag aaa acc atc tcc aaa gcc Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala	340	345	350		1056
aaa ggg cag ccc cga gaa cca cag gt <sup>g</sup> tac acc ctg ccc cca tcc cg <sup>g</sup> Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg	355	360	365		1104
gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly	370	375	380		1152
ttc tat ccc agc gac atc gcc gt <sup>g</sup> gag tgg gag agc aat ggg cag cg <sup>g</sup> Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro	385	390	395	400	1200
gag aac aac tac aag acc acg cct ccc gt <sup>g</sup> ctg gac tcc gac ggc tcc Glu Asn Asn Tyr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser	405	410	415		1248
ttc ttc ctc tac agc aag ctc acc gt <sup>g</sup> gac aag agc agg tgg cag cag Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln	420	425	430		1296
ggg aac gtc ttc tca tgc tcc gt <sup>g</sup> atg cat gag gct ctg cac aac cac Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His	435	440	445		1344
tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa ctg gtt ccg cgt Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Val Pro Arg	450	455	460		1392
ggt tcc gga tca ggt ggc cat cac cat cac cat cac					1428

Gly Ser Gly Ser Gly Gly His His His His His His  
 465                          470                          475

<210> 23

<211> 476

<212> PRT

<213> Homo sapiens

<400> 23

Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser  
 1                        5                        10                        15  
 Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val  
 20                        25                        30  
 Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly  
 35                        40                        45  
 Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp  
 50                        55                        60  
 Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser  
 65                        70                        75                        80  
 Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu  
 85                        90                        95  
 His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile  
 100                      105                        110  
 Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His  
 115                      120                        125  
 Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr  
 130                      135                        140  
 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys  
 145                      150                        155                        160  
 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu  
 165                      170                        175  
 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg  
 180                      185                        190  
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val  
 195                      200                        205  
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Gly Ser Gly Ser  
 210                      215                        220  
 Gly Ser Gly Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys Pro  
 225                      230                        235                        240  
 Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe  
 245                      250                        255

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
                  260                 265                 270  
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe  
                  275                 280                 285  
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro  
                  290                 295                 300  
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr  
                  305                 310                 315                 320  
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val  
                  325                 330                 335  
 Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala  
                  340                 345                 350  
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
                  355                 360                 365  
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
                  370                 375                 380  
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
                  385                 390                 395                 400  
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser  
                  405                 410                 415  
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln  
                  420                 425                 430  
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His  
                  435                 440                 445  
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Val Pro Arg  
                  450                 455                 460  
 Gly Ser Gly Ser Gly Gly His His His His His  
                  465                 470                 475

<210> 24

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC29328

<400> 24

tcagaggat ccggttcggg ttcgggttcg gagccagat catcagacaa aactcacaca  
tgc

60

63

<210> 25

<211> 65  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer ZC29231

<400> 25  
cgactgactc gagctactcc ataggcatat actcgccacc tgatccttta cccggagaca 60  
gggag 65

<210> 26  
<211> 70  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer ZC39335

<400> 26  
atcggaaattc gcagaagcca tgaggacgct gctgaccatc ttgactgtgg ggtccctggc 60  
tgctcacgcc 70

<210> 27  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer ZC28981

<400> 27  
tttgggctcc ctgagctctg gtggaa 26

<210> 28  
<211> 80  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer ZC39043

<400> 28

ctgactcgag ctactccata ggcataatact cgccacactga tccggAACCA cgcgAACCA  
gtttacccgg agacaggAGG 60  
80

<210> 29

<211> 1452

<212> DNA

<213> Artificial Sequence

<220>

<223> hzcytor11 extracellular cytokine binding domain  
fused to IgGg1 with a Glu-Glu tag

<221> CDS

<222> (1)...(1452)

<400> 29

atg	agg	acg	ctg	ctg	acc	atc	ttt	act	gtt	gga	tcc	ctg	gct	gct	cac		48
Met	Arg	Thr	Leu	Leu	Thr	Ile	Leu	Thr	Val	Gly	Ser	Leu	Ala	Ala	His		
1	5					10							15				

gcc	cct	gag	gac	ccc	tcg	gat	ctg	ctc	cag	cac	gtt	aaa	ttt	cag	tcc		96
Ala	Pro	Glu	Asp	Pro	Ser	Asp	Leu	Leu	Gln	His	Val	Lys	Phe	Gln	Ser		
20						25											

agc	aac	ttt	gaa	aac	atc	ctg	acg	tgg	gac	agc	ggg	cca	gag	ggc	acc		144
Ser	Asn	Phe	Glu	Asn	Ile	Leu	Thr	Trp	Asp	Ser	Gly	Pro	Glu	Gly	Thr		
35						40						45					

cca	gac	acg	gtc	tac	agc	atc	gag	tat	aag	acg	tac	gga	gag	agg	gac		192
Pro	Asp	Thr	Val	Tyr	Ser	Ile	Glu	Tyr	Lys	Thr	Tyr	Gly	Glu	Arg	Asp		
50						55						60					

tgg	gtt	gca	aag	aag	ggc	tgt	cag	cg	atc	acc	cg	aag	tcc	tgc	aac		240
Trp	Val	Ala	Lys	Lys	Gly	Cys	Gln	Arg	Ile	Thr	Arg	Lys	Ser	Cys	Asn		
65					70				75				80				

ctg	acg	gtt	gag	acg	ggc	aac	ctc	acg	gag	ctc	tac	tat	gcc	agg	gtc		288
Leu	Thr	Val	Glu	Thr	Gly	Asn	Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val		
85						90						95					

acc	gct	gtt	agt	gct	gga	ggc	cgg	tca	gcc	acc	aag	atg	act	gac	agg		336
Thr	Ala	Val	Ser	Ala	Gly	Gly	Arg	Ser	Ala	Thr	Lys	Met	Thr	Asp	Arg		
100						105						110					

ttc agc tct ctg cag cac act acc ctc aag cca cct gat gtg acc tgt Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys 115 120 125	384
atc tcc aaa gtg aga tcg att cag att gtt cat cct acc ccc acg Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr 130 135 140	432
cca atc cgt gca ggc gat ggc cac cg <sup>g</sup> cta acc ctg gaa gac atc ttc Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe 145 150 155 160	480
cat gac ctg ttc tac cac tta gag ctc cag gtc aac cgc acc tac caa His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln 165 170 175	528
atg cac ctt gga ggg aag cag aga gaa tat gag ttc ttc ggc ctg acc Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr 180 185 190	576
cct gac aca gag ttc ctt ggc acc atc atg att tgc gtt ccc acc tgg Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp 195 200 205	624
gcc aag gag agt gcc ccc tac atg tgc cga gtg aag aca ctg cca gac Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp 210 215 220	672
cg <sup>g</sup> aca tgg acc gga tcc ggt tcg ggt tcg gag ccc aga tca Arg Thr Trp Thr Gly Ser Gly Ser Gly Ser Glu Pro Arg Ser 225 230 235 240	720
tca gac aaa act cac aca tgc cca c <sup>g</sup> tgc cca gca cct gaa gcc gag Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu 245 250 255	768
ggg gca ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu 260 265 270	816
atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gac gtg agc	864

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser				
275	280	285		
cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag				912
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu				
290	295	300		
gtg cat aat gcc aag aca aag ccg cg <sup>g</sup> gag cag tac aac agc acg				960
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr				
305	310	315	320	
tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat				1008
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn				
325	330	335		
ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca tcc tcc				1056
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser				
340	345	350		
atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag				1104
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln				
355	360	365		
gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc				1152
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val				
370	375	380		
agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg				1200
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val				
385	390	395	400	
gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct				1248
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro				
405	410	415		
ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc				1296
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr				
420	425	430		
gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg				1344
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val				
435	440	445		

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg      1392  
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
 450                  455                  460

tct ccg ggt aaa ctg gtt ccg cgt ggt tcc gga tca ggt ggc gag tat      1440  
 Ser Pro Gly Lys Leu Val Pro Arg Gly Ser Gly Ser Gly Glu Tyr  
 465                  470                  475                  480

atg cct atg gag      1452  
 Met Pro Met Glu

<210> 30  
 <211> 484  
 <212> PRT  
 <213> Artificial Sequence

<400> 30  
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 1                5                10                15  
 Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser  
 20                25                30  
 Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr  
 35                40                45  
 Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp  
 50                55                60  
 Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn  
 65                70                75                80  
 Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val  
 85                90                95  
 Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg  
 100               105               110  
 Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys  
 115               120               125  
 Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr  
 130               135               140  
 Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe  
 145               150               155               160  
 His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln  
 165               170               175  
 Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr  
 180               185               190

Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp  
                  195                 200                 205  
 Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp  
                  210                 215                 220  
 Arg Thr Trp Thr Gly Ser Gly Ser Gly Ser Glu Pro Arg Ser  
                  225                 230                 235                 240  
 Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu  
                  245                 250                 255  
 Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
                  260                 265                 270  
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
                  275                 280                 285  
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
                  290                 295                 300  
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
                  305                 310                 315                 320  
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
                  325                 330                 335  
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser  
                  340                 345                 350  
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
                  355                 360                 365  
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val  
                  370                 375                 380  
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
                  385                 390                 395                 400  
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
                  405                 410                 415  
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr  
                  420                 425                 430  
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
                  435                 440                 445  
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
                  450                 455                 460  
 Ser Pro Gly Lys Leu Val Pro Arg Gly Ser Gly Ser Gly Gly Glu Tyr  
                  465                 470                 475                 480  
 Met Pro Met Glu

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC37693

&lt;400&gt; 31

cccccagacac ggtctacagc at

22

&lt;210&gt; 32

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC37449

&lt;400&gt; 32

gggtcaggcc gaagaactca tat

23

&lt;210&gt; 33

&lt;211&gt; 199

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 33

Met	Val	Pro	Pro	Pro	Glu	Asn	Val	Arg	Met	Asn	Ser	Val	Asn	Phe	Lys
1					5			10					15		
Asn	Ile	Leu	Gln	Trp	Glu	Ser	Pro	Ala	Phe	Ala	Lys	Gly	Asn	Leu	Thr
					20			25			30				
Phe	Thr	Ala	Gln	Tyr	Leu	Ser	Tyr	Arg	Ile	Phe	Gln	Asp	Lys	Cys	Met
					35			40			45				
Asn	Thr	Thr	Leu	Thr	Glu	Cys	Asp	Phe	Ser	Ser	Leu	Ser	Lys	Tyr	Gly
					50			55			60				
Asp	His	Thr	Leu	Arg	Val	Arg	Ala	Glu	Phe	Ala	Asp	Glu	His	Ser	Asp
65					70			75			80				
Trp	Val	Asn	Ile	Thr	Phe	Cys	Pro	Val	Asp	Asp	Thr	Ile	Ile	Gly	Pro
					85			90			95				
Pro	Gly	Met	Gln	Val	Glu	Val	Leu	Ala	Asp	Ser	Leu	His	Met	Arg	Phe
					100			105			110				
Leu	Ala	Pro	Lys	Ile	Glu	Asn	Glu	Tyr	Glu	Thr	Trp	Thr	Met	Lys	Asn
					115			120			125				
Val	Tyr	Asn	Ser	Trp	Thr	Tyr	Asn	Val	Gln	Tyr	Trp	Lys	Asn	Gly	Thr
					130			135			140				

Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg  
 145 150 155 160  
 Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu  
 165 170 175  
 Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln  
 180 185 190  
 Thr Thr His Asp Glu Thr Val  
 195

<210> 34  
 <211> 211  
 <212> PRT  
 <213> Homo sapiens

<400> 34  
 Ser Asp Ala His Gly Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe  
 1 5 10 15  
 Glu Ala Glu Phe Phe His His Ile Leu His Trp Thr Pro Ile Pro Asn  
 20 25 30  
 Gln Ser Glu Ser Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile  
 35 40 45  
 Glu Ser Trp Asn Ser Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp  
 50 55 60  
 Leu Thr Ala Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala  
 65 70 75 80  
 Arg Val Arg Ala Val Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr  
 85 90 95  
 Asn Thr Arg Phe Ser Val Asp Glu Val Thr Leu Thr Val Gly Ser Val  
 100 105 110  
 Asn Leu Glu Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro  
 115 120 125  
 Arg Pro Lys Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser  
 130 135 140  
 His Phe Arg Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe  
 145 150 155 160  
 Thr Phe Thr His Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr  
 165 170 175  
 Ser Gly Glu Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala  
 180 185 190  
 Ser Arg Ser Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu  
 195 200 205

Thr Arg Gln

210

<210> 35

<211> 201

<212> PRT

<213> Homo sapiens

<400> 35

Asp	Glu	Val	Ala	Ile	Leu	Pro	Ala	Pro	Gln	Asn	Leu	Ser	Val	Leu	Ser
1				5					10					15	
Thr	Asn	Met	Lys	His	Leu	Leu	Met	Trp	Ser	Pro	Val	Ile	Ala	Pro	Gly
		20					25						30		
Glu	Thr	Val	Tyr	Tyr	Ser	Val	Glu	Tyr	Gln	Gly	Glu	Tyr	Glu	Ser	Leu
			35			40					45				
Tyr	Thr	Ser	His	Ile	Trp	Ile	Pro	Ser	Ser	Trp	Cys	Ser	Leu	Thr	Glu
			50			55				60					
Gly	Pro	Glu	Cys	Asp	Val	Thr	Asp	Asp	Ile	Thr	Ala	Thr	Val	Pro	Tyr
	65				70				75				80		
Asn	Leu	Arg	Val	Arg	Ala	Thr	Leu	Gly	Ser	Gln	Thr	Ser	Ala	Trp	Ser
				85				90			95				
Ile	Leu	Lys	His	Pro	Phe	Asn	Arg	Asn	Ser	Thr	Ile	Leu	Thr	Arg	Pro
				100			105					110			
Gly	Met	Glu	Ile	Thr	Lys	Asp	Gly	Phe	His	Leu	Val	Ile	Glu	Leu	Glu
			115			120				125					
Asp	Leu	Gly	Pro	Gln	Phe	Glu	Phe	Leu	Val	Ala	Tyr	Trp	Arg	Arg	Glu
				130			135			140					
Pro	Gly	Ala	Glu	Glu	His	Val	Lys	Met	Val	Arg	Ser	Gly	Gly	Ile	Pro
	145				150				155				160		
Val	His	Leu	Glu	Thr	Met	Glu	Pro	Gly	Ala	Ala	Tyr	Cys	Val	Lys	Ala
				165			170				175				
Gln	Thr	Phe	Val	Lys	Ala	Ile	Gly	Arg	Tyr	Ser	Ala	Phe	Ser	Gln	Thr
			180			185				190					
Glu	Cys	Val	Glu	Val	Gln	Gly	Glu	Ala							
			195			200									

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